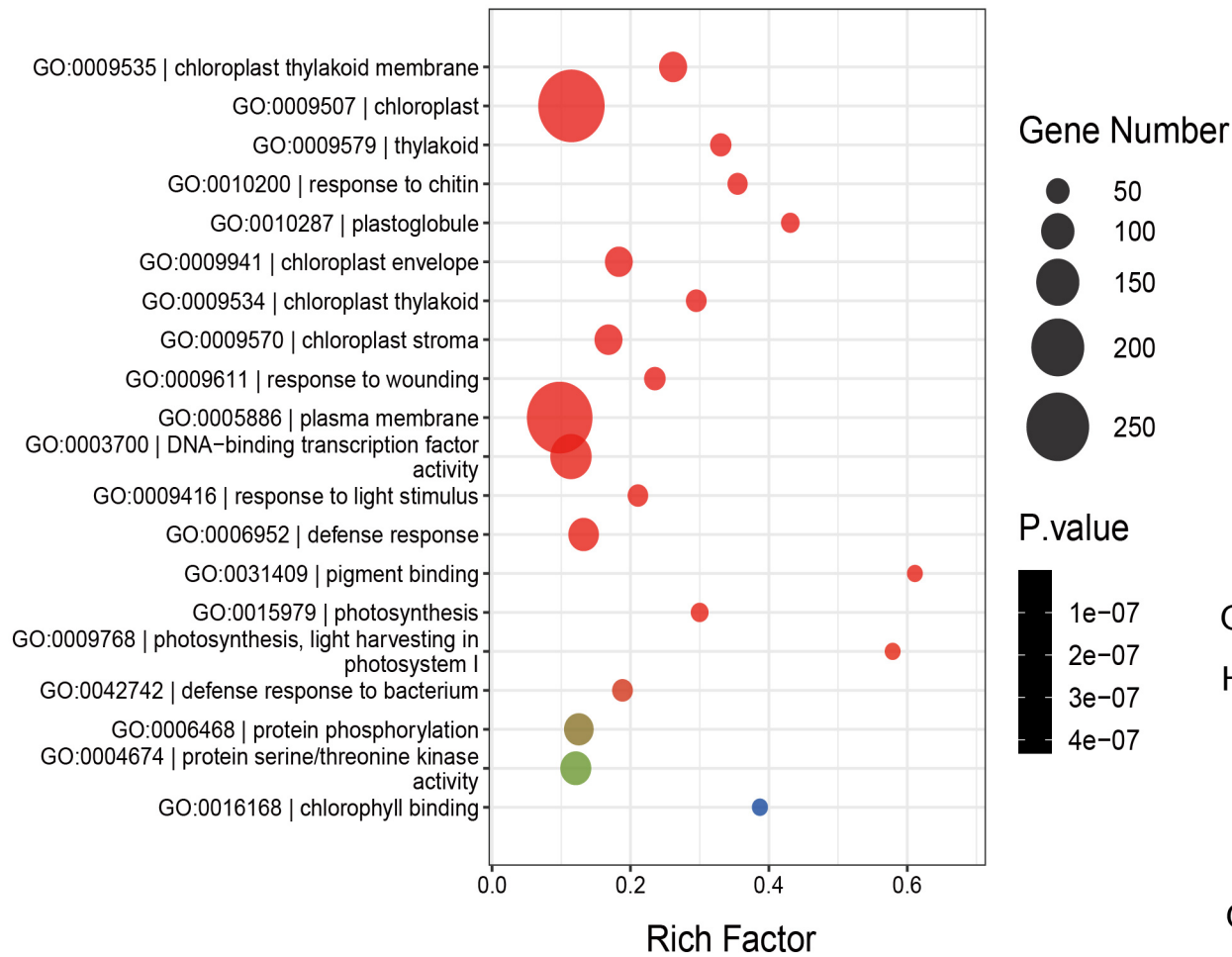


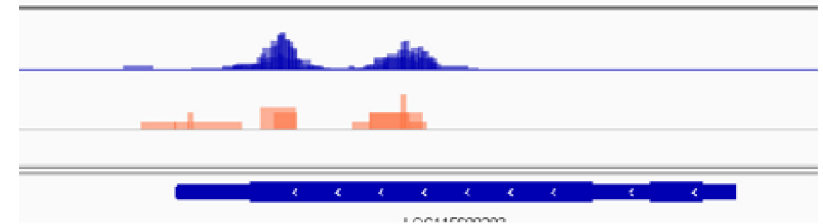
A

GO Enrichment Scatter Plot

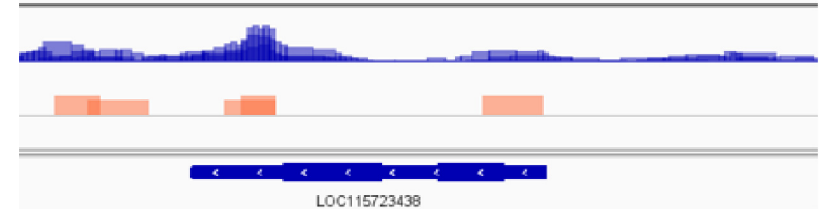
GO Term

**B**

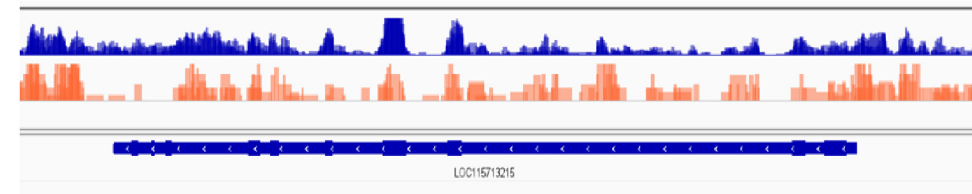
LOC115699293 TKS1-1

O
H

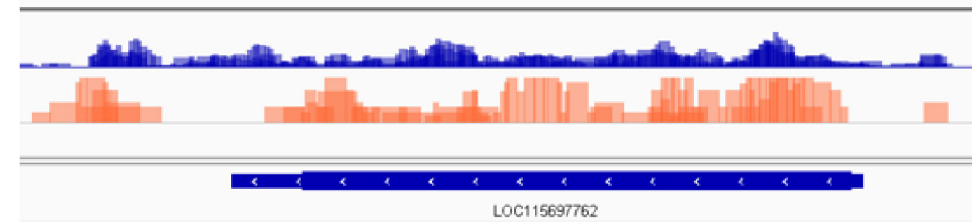
LOC115723438 OAC-2

O
H

LOC115713215 PT13

O
H

LOC115697762 CBDAS5

O
H

Supplementary figure3: Integration of metabolome, transcriptome, and ATAC-seq data.

A. GO enrichment of Hyper-down gene.

B. Peak identified in cannabinoid biosynthesis pathway genes.